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To:

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25. Nov. 2003

Patentanwälte  
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|  |  |
|--|--|
| Date of mailing (day/month/year)<br>19 November 2003 (19.11.03)      | <b>IMPORTANT NOTIFICATION</b>  |
| Applicant's or agent's file reference<br>12186WO                     |  |
| International application No.<br>PCT/EP03/09968                      | International filing date (day/month/year)<br>08 September 2003 (08.09.03) |
| International publication date (day/month/year)<br>Not yet published | Priority date (day/month/year)<br>11 September 2002 (11.09.02)             |
| Applicant<br>ESPLORA GMBH et al                                      |  |

- The applicant is hereby notified of the date of receipt (except where the letters "NR" appear in the right-hand column) by the International Bureau of the priority document(s) relating to the earlier application(s) indicated below. Unless otherwise indicated by an asterisk appearing next to a date of receipt, or by the letters "NR", in the right-hand column, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).
- This updates and replaces any previously issued notification concerning submission or transmittal of priority documents.
- An asterisk(\*) appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b). In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.
- The letters "NR" appearing in the right-hand column denote a priority document which was not received by the International Bureau or which the applicant did not request the receiving Office to prepare and transmit to the International Bureau, as provided by Rule 17.1(a) or (b), respectively. In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

| <u>Priority date</u>      | <u>Priority application No.</u> | <u>Country or regional Office<br/>or PCT receiving Office</u> | <u>Date of receipt<br/>of priority document</u> |
|---------------------------|---------------------------------|---|---|
| 11 Sept 2002 (11.09.02) ✓ | 102 42 016.5 ✓                  | DE ✓  | 14 Nove 2003 (14.11.03)                         |

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|---|--|
| The International Bureau of WIPO<br>34, chemin des Colombettes<br>1211 Geneva 20, Switzerland<br><br>Facsimile No. (41-22) 338-7080 | Authorized officer<br><br>Chantal AUMAITRE<br><br>Telephone No. (41-22) 338 8669 |
|---|--|

SEQUENCE LISTING

<110> FrankGen Biotechnologie AG

<120> Method for identifying BBB-specific proteins and fragments thereof

<130> 12186WO

<140>

<141>

<160> 58

<170> PatentIn Ver. 2.1

<210> 1

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Clone S129 from BMEC from swine brain

<400> 1

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| ctgcagccga | ggacaacact | gattcgagcc | gtgacctacc | ggccgcggga | attcgattta | 60  |
| tgggtgaaat | cgccttcaat | acacccgcag | cggtgcaaaa | agaggaggcg | cagcaagacg | 120 |
| tgagggccct | cgtaagccat | acggtccgtg | ctcagatcct | gactggcaag | gaactccaag | 180 |
| ttgccactaa | ggaaaaagag | ggcttctctg | ggagatgcat | gcttactctc | gtaggccttt | 240 |
| ccttcattct | ggcaggactt | attgttggtg | gagcctgcat | ttacaagtac | ttcatgcca  | 300 |
| agagtaccat | actaccatgg | aga        |            |            |            | 323 |

<210> 2

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2

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| acctccattg | ttatgcctcc | ta | 22 |
|------------|------------|----|----|

<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

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| gttgccctctc | actcttgaca | ga | 22 |
|-------------|------------|----|----|

<210> 4

<211> 1598

<212> DNA

<213> Swine

<220>

<221> CDS

<222> (119)..(910)

<400> 4

gcggccgcta gcataaagaa ggtgattcta agcctagcgc tatcttctcc tagtccagcc 60  
 tgcagccgag gacaacactg attcgagccg tgacctaccg gccgcgggaa ttcgattt 118  
 atg gtg aaa atc gcc ttc aat aca ccc gca gcg gtg caa aaa gag gag 166  
 Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu  
 1 5 10 15  
 gcg cag caa gac gtg gag gcc ctc gta agc cat acg gtc cgt gct cag 214  
 Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln  
 20 25 30  
 atc ctg act ggc aag gaa ctc caa gtt gcc act aag gaa aaa gag ggc 262  
 Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly  
 35 40 45  
 ttc tct ggg aga tgc atg ctt act ctc gta ggc ctt tcc ttc atc ttg 310  
 Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu  
 50 55 60  
 gca gga ctt att gtt ggt gga gcc tgc att tac aag tac ttc atg ccc 358  
 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro  
 65 70 75 80  
 aag agt acc atc tac cat gga gag atg tgc ttc ttt gat tct gcg gac 406  
 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp  
 85 90 95  
 cct gca aat ttc ctc caa gga gga gag ccc tac ttc ctg cct gtg atg 454  
 Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met  
 100 105 110  
 gaa gag gct gat att cgt gaa gat gac aac att gca atc att gat gtg 502  
 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val  
 115 120 125  
 cct gtc ccc agt ttc tct gat agt gac cct gca gca att att cat gac 550  
 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp  
 130 135 140  
 ttt gaa aag ggc atg act gct tac ctg gac ttg ctg ctg ggg aac tgc 598  
 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys  
 145 150 155 160  
 tat ctg atg ccc ctc aat acc tcc att gtt atg cct cct aag tat ctc 646  
 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu  
 165 170 175  
 gtg gag ctc ttt ggc aaa ctg gca cgt ggc aaa tac ctc cct cac gct 694  
 Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala  
 180 185 190  
 tat gtg gtt cat gaa gac ctg gtt gct gtg gaa gag att cat gat gtt 742  
 Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val  
 195 200 205  
 agt aac ctt ggc atc ttt att tac caa ctt tgc aac aac cgc aag tct 790  
 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser  
 210 215 220  
 ttc cgc ctt cgt aga aga gac ctc ttg ctg ggt ttc aac aaa cgt gcc 838  
 Phe Arg Leu Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala  
 225 230 235 240  
 att gat aag tgc tgg aag att aga cac ttc ccc aat gaa ttt att gtt 886  
 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val  
 245 250 255

gag acc aag atc tgt caa gag tga gaggcaacag aaaaagagtg tacttagtaa 940  
 Glu Thr Lys Ile Cys Gln Glu  
 260

taggaagtca aagattttaca atatgacttc aatatttaaag tgtgtaggac attcaagata 1000  
 ttactcatg catttctctt attgcttata cttaaaaaaa agaaagaaaa taaaaactac 1060  
 taaccattgc aaaaaaaaaa aaaaaaagta ctagtcgacg cgtggccaga aactgaaatg 1120  
 aaatgatttt tatgtttttc cttttgaatt tatagggttt atgttttntt gaatgcaatg 1180  
 tgaagggtgt ggctaacatc ctgacaatga attccatccc ttgtgtatat gtgtgtcttt 1240  
 aaaagtaaaa tyttcartca tatggtaaaa catgttttaa atttaaaata tttaaaattg 1300  
 ttttcaacct ttttgtgtag cgcttgtcaa atatcttaac attgtcttgt tttgttttca 1360  
 ttgtgtgcaa ctttctgaa tttagaaatt aaatttttgc atttatgtta ggtgttctgt 1420  
 aatagatatg acttatatgt gaaaaacttt cataaagaag tcattttcac taatrcagtg 1480  
 actctcactg gtaactgtat tgtgaaatgc acaaaactgt tttagtgtg aatgctataa 1540  
 ggaatttagg ttgtatgaat tctacaatcc tataataaat ttaccatat tcaaaaaa 1598

<210> 5  
 <211> 263  
 <212> PRT  
 <213> Swine

<400> 5  
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 1 5 10 15  
 Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln  
 20 25 30  
 Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly  
 35 40 45  
 Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu  
 50 55 60  
 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro  
 65 70 75 80  
 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp  
 85 90 95  
 Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met  
 100 105 110  
 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val  
 115 120 125  
 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp  
 130 135 140  
 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Gly Asn Cys  
 145 150 155 160  
 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu  
 165 170 175  
 Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala  
 180 185 190  
 Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val  
 195 200 205  
 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser  
 210 215 220  
 Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala  
 225 230 235 240  
 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val  
 245 250 255  
 Glu Thr Lys Ile Cys Gln Glu  
 260

<210> 6  
 <211> 814  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Clone S231  
 from BMEC from swine brain

<400> 6  
 acatttcttt aggttcattc tggttaaggg gatgttcgag ggtggggccac caaattgtct 60  
 gggctgggga taaagcagtt ggcaagcaaa aactatggga tgatgaactt ttcaatwatg 120  
 atttaatgat cacatgagta tagaaagctg ttttgagtgc tgaaacagac ttacctatca 180  
 gatatatcca aaagagattc tatgttaaaa agtcagacta tgactggagt gaaccatgta 240  
 ttcccttgtc ttttactttg tttctgtgac atttatgttt catgtaactt gcattatggt 300  
 tgggtggggtt gtcctagtac tgtattttgg cttcttcttt aataggattg atatttcata 360  
 tabtataatt gtgaatattt tgakacraat gtttataact ctaggcatat aaaaacagat 420  
 tctgattccc ttcactgtgt gaatgttttc tgttgaaaaa atggaggata aatatggata 480  
 ctaatgacac tcattcctaa ttaagttttc aatcagtttg atttggataa cttgcattta 540  
 tccgagatat tgagctactt tctgataatg catcaagcat ttctaccata actctttcac 600  
 gcaactgaat gttgttaagt atagttttat cttgctttta ttaaacttct taagcaaaaa 660  
 aaaagaaact tcataagcta atacattaga gaaagggtat gatcttgaat cnagaatggc 720  
 ttatggcatt aaggaatgag atacttgtaa attttctttg aaacagccaa ctcctctgtt 780  
 gtgtcttcac aattcaaaa atatgcctca ctgt 814

<210> 7  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 ccataactct ttcacgcaac tg 22

<210> 8  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 acaacagagg agttggctgt tt 22

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 ggtattgctg gctggtatct tt 22

<210> 10  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

atgtaggaat agccgtggtg at

22

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

ggtctttgtg ttccagctct tc

22

<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

ttctcaggac cagatagaga acg

23

<210> 13

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Clone S231  
from BMEC from swine brain

<220>

<221> CDS

<222> (1)..(480)

<400> 13

atg ttg gtg tta ctg gct ggt atc ttt gtg gtc cac atc gcc act gtc 48  
Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val 15

gtc atg ctg ttc gtt tgc acc att gcc aat gtc tgg gtg gtc tca gat 96  
Val Met Leu Phe Val Cys Thr Ile Ala Asn Val Trp Val Val Ser Asp 30

gcg gga caa gga tct gtc ggt ctt tgg aaa aac tgt acc agt gct ggc 144  
Ala Gly Gln Gly Ser Val Gly Leu Trp Lys Asn Cys Thr Ser Ala Gly 45

tgt act gat acc ctg tta tac ggc ggt gaa gat gcc ctc aag tcg gtg 192  
Cys Thr Asp Thr Leu Leu Tyr Gly Gly Glu Asp Ala Leu Lys Ser Val 60

cag gcc ttc atg atc ctg tct atc atc ttc tct gtc gtc tcc ctc gtg 240  
Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Val Val Ser Leu Val 80

|   |     |
|---|-----|
| gtc ttt gtg ttc cag ctc ttc acc atg gag aaa ggc aac cgc ttc ttc | 288 |
| Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe |     |
| 85 90 95  |     |
| ctc tcg gga gcc acc atg ctg gtg tgc tgg ctg tgc atc atg gtg ggg | 336 |
| Leu Ser Gly Ala Thr Met Leu Val Cys Trp Leu Cys Ile Met Val Gly |     |
| 100 105 110   |     |
| gcc tcc gtc tat act cat cat tat gcc aac agt tct aaa aac caa tac | 384 |
| Ala Ser Val Tyr Thr His His Tyr Ala Asn Ser Ser Lys Asn Gln Tyr |     |
| 115 120 125   |     |
| tcg gcg agt cac cat ggc tat tcc ttc atc ctc gcc tgg atc tgc ttc | 432 |
| Ser Ala Ser His His Gly Tyr Ser Phe Ile Leu Ala Trp Ile Cys Phe |     |
| 130 135 140   |     |
| tgc ttc agc ttc atc atc ggc gtt ctc tat ctg gtc ctg aga aag aaa | 480 |
| Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys |     |
| 145 150 155 160   |     |
| taa   | 483 |

<210> 14  
 <211> 160  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: Clone S231  
 from BMEC from swine brain

<400> 14  
 Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val  
 1 5 10 15  
 Val Met Leu Phe Val Cys Thr Ile Ala Asn Val Trp Val Val Ser Asp  
 20 25 30  
 Ala Gly Gln Gly Ser Val Gly Leu Trp Lys Asn Cys Thr Ser Ala Gly  
 35 40 45  
 Cys Thr Asp Thr Leu Leu Tyr Gly Gly Glu Asp Ala Leu Lys Ser Val  
 50 55 60  
 Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Val Val Ser Leu Val  
 65 70 75 80  
 Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe  
 85 90 95  
 Leu Ser Gly Ala Thr Met Leu Val Cys Trp Leu Cys Ile Met Val Gly  
 100 105 110  
 Ala Ser Val Tyr Thr His His Tyr Ala Asn Ser Ser Lys Asn Gln Tyr  
 115 120 125  
 Ser Ala Ser His His Gly Tyr Ser Phe Ile Leu Ala Trp Ile Cys Phe  
 130 135 140  
 Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys  
 145 150 155 160

<210> 15  
 <211> 513  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Clone S012  
from BMEC from swine brain

<400> 15

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gggatgtcat cgctattgtt agaatactga catcactttt ctgagcagaa attgaaactg 120
taaattttaac cttttaatta tcacctcacc tgaaaagggt ggttgagata ctcacgcagc 180
atgtattata ttaaccatgt catgtttaag ttattaaatt cagattattt ataacttatt 240
atcttagggc ctgcctcatg tcttctaggg tatttgagta atcatcctat atttaaagtt 300
aaaactttga cttaaaaaac actgttaatg aaagttccct agcgcttttc ttattttcaa 360
attggcttta tgggtagtag tagagaattc catgctgttc tgaggctagc ttccaggtaa 420
acagtgattt ttttttctt tttttcttc tttcttgggt agtggtccag agttttaagc 480
tacttttctc aaagtttcaa ccctttccca ggt 513
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<210> 16

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

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gtatcgggag tggaggatta ca 22
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<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

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cccgaggtat atttgtttct gg 22
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<210> 18

<211> 1674

<212> DNA

<213> Swine

<220>

<221> CDS

<222> (40)..(774)

<400> 18

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ccgtctgcct ggtcccarag gcgcaccggc ttcggtaac atg ttt gtg gca gct 54
                               Met Phe Val Ala Ala
                               1 5
```

```
cgg aca ggc cag aga acc ttg aga aag gtg gtc tcg gga tgc cgt cca 102
Arg Thr Gly Gln Arg Thr Leu Arg Lys Val Val Ser Gly Cys Arg Pro
          10          15          20
```

```
aaa tcg gcg aca gcg act gga gtc ccg gct cct gcg cag ggg cct ccg 150
Lys Ser Ala Thr Ala Thr Gly Val Pro Ala Pro Ala Gln Gly Pro Pro
          25          30          35
```

```
cgg aac atc aga tac tta gcc tcc tgt ggt ata ctg atg aac aga act 198
Arg Asn Ile Arg Tyr Leu Ala Ser Cys Gly Ile Leu Met Asn Arg Thr
          40          45          50
```



|             |             |            |             |             |            |     |     |     |     |     |     |     |     |     |     |      |
|-------------|-------------|------------|-------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ctt         | cca         | ctg        | cat         | tcc         | tca        | ttt | ttg | cct | aag | gag | atg | tat | gca | aga | acc | 246  |
| Leu         | Pro         | Leu        | His         | Ser         | Ser        | Phe | Leu | Pro | Lys | Glu | Met | Tyr | Ala | Arg | Thr |      |
|             | 55          |            |             |             |            | 60  |     |     |     |     | 65  |     |     |     |     |      |
| ttc         | ttc         | aga        | att         | gct         | gca        | cca | tta | ata | aac | aaa | aga | aaa | gaa | tat | tca | 294  |
| Phe         | Phe         | Arg        | Ile         | Ala         | Ala        | Pro | Leu | Ile | Asn | Lys | Arg | Lys | Glu | Tyr | Ser |      |
| 70          |             |            |             |             | 75         |     |     |     |     | 80  |     |     |     |     | 85  |      |
| gag         | agg         | agg        | att         | ata         | gga        | tat | tct | atg | cag | gaa | atg | tat | gac | gta | gta | 342  |
| Glu         | Arg         | Arg        | Ile         | Ile         | Gly        | Tyr | Ser | Met | Gln | Glu | Met | Tyr | Asp | Val | Val |      |
|             |             |            |             | 90          |            |     |     |     | 95  |     |     |     |     | 100 |     |      |
| tcg         | gga         | atg        | gaa         | gat         | tac        | aag | cat | ttt | gtg | cct | tgg | tgc | aaa | aaa | tca | 390  |
| Ser         | Gly         | Met        | Glu         | Asp         | Tyr        | Lys | His | Phe | Val | Pro | Trp | Cys | Lys | Lys | Ser |      |
|             |             |            | 105         |             |            |     |     | 110 |     |     |     |     | 115 |     |     |      |
| gat         | gta         | ata        | tca         | agg         | aga        | tct | gga | tac | tgc | aaa | aca | cga | tta | gaa | att | 438  |
| Asp         | Val         | Ile        | Ser         | Arg         | Arg        | Ser | Gly | Tyr | Cys | Lys | Thr | Arg | Leu | Glu | Ile |      |
|             |             | 120        |             |             |            |     | 125 |     |     |     |     | 130 |     |     |     |      |
| ggg         | ttt         | cca        | ccc         | gta         | ttg        | gag | cgc | tat | acg | tca | gta | gta | acc | ttg | gtg | 486  |
| Gly         | Phe         | Pro        | Pro         | Val         | Leu        | Glu | Arg | Tyr | Thr | Ser | Val | Val | Thr | Leu | Val |      |
|             | 135         |            |             |             |            | 140 |     |     |     |     | 145 |     |     |     |     |      |
| aaa         | cca         | cat        | ttg         | gta         | aag        | gca | tcc | tgt | gca | gat | ggg | aag | ctc | ttt | aat | 534  |
| Lys         | Pro         | His        | Leu         | Val         | Lys        | Ala | Ser | Cys | Ala | Asp | Gly | Lys | Leu | Phe | Asn |      |
| 150         |             |            |             |             | 155        |     |     |     |     | 160 |     |     |     |     | 165 |      |
| cac         | tta         | gag        | act         | gtt         | tgg        | cgt | ttt | agc | cca | ggt | ctt | cct | ggc | tac | cca | 582  |
| His         | Leu         | Glu        | Thr         | Val         | Trp        | Arg | Phe | Ser | Pro | Gly | Leu | Pro | Gly | Tyr | Pro |      |
|             |             |            |             | 170         |            |     |     |     | 175 |     |     |     |     | 180 |     |      |
| aga         | act         | tgt        | act         | ttg         | gat        | ttt | tca | att | tct | ttt | gaa | ttt | cga | tca | ctt | 630  |
| Arg         | Thr         | Cys        | Thr         | Leu         | Asp        | Phe | Ser | Ile | Ser | Phe | Glu | Phe | Arg | Ser | Leu |      |
|             |             |            | 185         |             |            |     | 190 |     |     |     |     |     | 195 |     |     |      |
| ctg         | cac         | tct        | cag         | ctt         | gcc        | aca | ttg | ttt | ttt | gat | gaa | gtt | gtg | aag | cag | 678  |
| Leu         | His         | Ser        | Gln         | Leu         | Ala        | Thr | Leu | Phe | Phe | Asp | Glu | Val | Val | Lys | Gln |      |
|             |             | 200        |             |             |            | 205 |     |     |     |     |     | 210 |     |     |     |      |
| atg         | gta         | gct        | gct         | ttt         | gaa        | aga | aga | gca | tgt | aaa | ctg | tat | ggt | cca | gaa | 726  |
| Met         | Val         | Ala        | Ala         | Phe         | Glu        | Arg | Arg | Ala | Cys | Lys | Leu | Tyr | Gly | Pro | Glu |      |
|             | 215         |            |             |             |            | 220 |     |     |     |     | 225 |     |     |     |     |      |
| aca         | agt         | ata        | cct         | cgg         | gaa        | tta | atg | ctt | cat | gaa | gtt | cat | cac | aca | taa | 774  |
| Thr         | Ser         | Ile        | Pro         | Arg         | Glu        | Leu | Met | Leu | His | Glu | Val | His | His | Thr |     |      |
| 230         |             |            |             | 235         |            |     |     |     |     | 240 |     |     |     |     | 245 |      |
| gagaaaagga  | aatgggtgccc | tacttgtaac | tagttttattc | acttttagga  | agtgctttca |     |     |     |     |     |     |     |     |     |     | 834  |
| tcatttttgct | ytcagaaggc  | agaaagcatt | tgtcaaacac  | agctttgata  | taaacctgta |     |     |     |     |     |     |     |     |     |     | 894  |
| ctttgcactt  | ggaatatgga  | accacatgta | catagaattc  | aatcaagtgt  | aattcagaat |     |     |     |     |     |     |     |     |     |     | 954  |
| aatgtgtata  | ttagcatatt  | tacagtaatg | ggatgtcatc  | gctattgtta  | gaatactgac |     |     |     |     |     |     |     |     |     |     | 1014 |
| atcacttttc  | tgagcagaaa  | ttgaaactgt | aaatttaacc  | ttttaattat  | cacctcacct |     |     |     |     |     |     |     |     |     |     | 1074 |
| gaaaagggttg | gttgagatac  | tcacgcagca | tgtattatat  | taaccatgtc  | atgtttaagt |     |     |     |     |     |     |     |     |     |     | 1134 |
| tattaaattc  | agattattta  | taacttatta | tcttagggcc  | tgccctcatgt | cttctagggt |     |     |     |     |     |     |     |     |     |     | 1194 |
| atgtgagtaa  | tcacccata   | tttaaagtta | aaactttgac  | ttaaaaaca   | ctgttaatga |     |     |     |     |     |     |     |     |     |     | 1254 |
| aagttcccta  | gcgcttttct  | tattttcaaa | ttgggtcttat | gggtagtagt  | agagaattcc |     |     |     |     |     |     |     |     |     |     | 1314 |
| atgctgttct  | gaggctagct  | tccaggtaaa | cagtgatttt  | ttttttcttt  | ttttctttct |     |     |     |     |     |     |     |     |     |     | 1374 |

ttcttggtga gtggtccaga gttttaagct acttttctca aagtttcaac cctttcccag 1434  
 gtacttttgac tactatttca gtaatgttga ttgtgtgtca agttttgtct acagcagtgg 1494  
 gcaatagatg aaggaagtcg gttgatatgt ctccaacacc atgcattctg attttctatt 1554  
 tattgtgtat actcactttc aataatgtat ttccaactga tatttttgta aacaaatcag 1614  
 tgtaaggact gaagtggtaa cttaataaag ttaatttggt taaaaataa aaaaaaaaaa 1674

<210> 19  
 <211> 244  
 <212> PRT  
 <213> Swine

<400> 19  
 Met Phe Val Ala Ala Arg Thr Gly Gln Arg Thr Leu Arg Lys Val Val  
 1 5 10 15  
 Ser Gly Cys Arg Pro Lys Ser Ala Thr Ala Thr Gly Val Pro Ala Pro  
 20 25 30  
 Ala Gln Gly Pro Pro Arg Asn Ile Arg Tyr Leu Ala Ser Cys Gly Ile  
 35 40 45  
 Leu Met Asn Arg Thr Leu Pro Leu His Ser Ser Phe Leu Pro Lys Glu  
 50 55 60  
 Met Tyr Ala Arg Thr Phe Phe Arg Ile Ala Ala Pro Leu Ile Asn Lys  
 65 70 75 80  
 Arg Lys Glu Tyr Ser Glu Arg Arg Ile Ile Gly Tyr Ser Met Gln Glu  
 85 90 95  
 Met Tyr Asp Val Val Ser Gly Met Glu Asp Tyr Lys His Phe Val Pro  
 100 105 110  
 Trp Cys Lys Lys Ser Asp Val Ile Ser Arg Arg Ser Gly Tyr Cys Lys  
 115 120 125  
 Thr Arg Leu Glu Ile Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser  
 130 135 140  
 Val Val Thr Leu Val Lys Pro His Leu Val Lys Ala Ser Cys Ala Asp  
 145 150 155 160  
 Gly Lys Leu Phe Asn His Leu Glu Thr Val Trp Arg Phe Ser Pro Gly  
 165 170 175  
 Leu Pro Gly Tyr Pro Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe  
 180 185 190  
 Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp  
 195 200 205  
 Glu Val Val Lys Gln Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys  
 210 215 220  
 Leu Tyr Gly Pro Glu Thr Ser Ile Pro Arg Glu Leu Met Leu His Glu  
 225 230 235 240  
 Val His His Thr

<210> 20  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 20  
 cgcgtggtga atgatctgta

20

<210> 21  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21  
ctccatgatc aggtcctcca g 21

<210> 22  
<211> 607  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Partial  
CDNA sequence of NSE2 from swine

<220>  
<221> CDS  
<222> (1)..(192)

<400> 22  
gag gac ctg atc atg gag aaa cgg cgc aac gac cag ata ggg cgc gcc 48  
Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala  
1 5 10 15  
gcg gtg cta cag gag ctg gcc acg cac ctg cac ccc gcg gag ccg gac 96  
Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp  
20 25 30  
gag ggc gac agc gac gcc gcg cgg act acg ccg cct ccc ggg cgc tcc 144  
Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser  
35 40 45  
cag gcg ccg ggc caa gag gag gag gac cga gag gcg gtg gtg cac tga 192  
Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His  
50 55 60  
caggcgagct gagtgcggag ctgcgtgagg gagcctttgc agcagccgct gccccctccc 252  
ttctctccct ccctcctcca ccatcttctg ggtcccaact gggctcctgg gccatttgga 312  
aaacggagag ttggcgaaaa gcgctgccag ctgtggcttg agtttggttat cttggacgga 372  
ggaggaagag ggagcagctt ccatggaccc ctgatcacta cttgaggaga attttcctgt 432  
ggattcaact gactagctat tgtgatgtaa gcagtttgag gtgactggcc cagcaggagt 492  
gagaagaatt tatcttcagc ataaacttca ttattctaca gtgtttcttc atttgcctga 552  
gaggtaaagga tgctatgtag acagaaacaa aggaagaaaa aaaaaaaaaa aaaaa 607

<210> 23  
<211> 63  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: Partial  
CDNA sequence of NSE2 from swine

<400> 23  
Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala  
1 5 10 15  
Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp  
20 25 30  
Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser  
35 40 45  
Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His  
50 55 60

<210> 24  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 24  
 cgagaccctg tgggtggctta ttac 24

<210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 25  
 ctggtgtatt agctggagcg tgtg 24

<210> 26  
 <211> 586  
 <212> DNA  
 <213> Swine

<220>  
 <221> CDS  
 <222> (1)..(585)

<400> 26  
 cga gac cct gtg gtg gct tat tac tgt cgt tta tat gca atg caa act 48  
 Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr  
 1 5 10 15

gga atg aag att gat agt aaa act cct gaa tgt cgt aaa ttt tta tca 96  
 Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser  
 20 25 30

aag ctg atg gat cag tta gaa gct ctt aag aaa cag ttg ggt gac aat 144  
 Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn  
 35 40 45

gaa gct gtt act caa gaa ata gtt ggt tct gcc cac ttg gag aat tat 192  
 Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr  
 50 55 60

gct ttg aaa atg ttt tta tat gca gat aat gaa gat cgg gct ggg cga 240  
 Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg  
 65 70 75 80

ttt cat aaa aac atg atc aag tcc ttc tat act gca agt ctt tta ata 288  
 Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile  
 85 90 95

gat gtc ata aca gtg ttt gga gaa ctc act gat gaa aat gtg aaa cac 336  
 Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His  
 100 105 110

aga aag tat gca agg tgg aag gca aca tat att cat aat tgt tta aag 384  
 Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys  
 115 120 125

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| aat<br>Asn | gga<br>Gly | ggg<br>Gly | act<br>Thr | cct<br>Pro | caa<br>Gln | gca<br>Ala | ggt<br>Gly | cct<br>Pro | gtg<br>Val | ggc<br>Gly | att<br>Ile | gaa<br>Glu | gaa<br>Glu | gat<br>Asp | aat<br>Asn | 432 |
| 130        |            |            |            |            |            | 135        |            |            |            |            | 140        |            |            |            |            |     |
| gac<br>Asp | ata<br>Ile | gaa<br>Glu | gaa<br>Glu | aat<br>Asn | gaa<br>Glu | gat<br>Asp | gct<br>Ala | gga<br>Gly | gca<br>Ala | acc<br>Thr | tct<br>Ser | ctg<br>Leu | ccc<br>Pro | act<br>Thr | cag<br>Gln | 480 |
| 145        |            |            |            |            | 150        |            |            |            |            | 155        |            |            |            |            | 160        |     |
| cca<br>Pro | cct<br>Pro | cag<br>Gln | cca<br>Pro | tca<br>Ser | tct<br>Ser | tcc<br>Ser | act<br>Thr | tat<br>Tyr | gac<br>Asp | cca<br>Pro | ggc<br>Gly | aac<br>Asn | atg<br>Met | cca<br>Pro | tcg<br>Ser | 528 |
|            |            |            |            | 165        |            |            |            |            | 170        |            |            |            |            | 175        |            |     |
| agc<br>Ser | agc<br>Ser | tat<br>Tyr | act<br>Thr | gga<br>Gly | ata<br>Ile | cag<br>Gln | att<br>Ile | cct<br>Pro | ccc<br>Pro | ggt<br>Gly | gca<br>Ala | cac<br>His | gct<br>Ala | cca<br>Pro | gct<br>Ala | 576 |
|            |            |            | 180        |            |            |            |            | 185        |            |            |            |            | 190        |            |            |     |
| aat<br>Asn | aca<br>Thr | cca<br>Pro | g          |            |            |            |            |            |            |            |            |            |            |            |            | 586 |
|            |            | 195        |            |            |            |            |            |            |            |            |            |            |            |            |            |     |

<210> 27  
 <211> 195  
 <212> PRT  
 <213> Swine

<400> 27  
 Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr  
 1 5 10 15  
 Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser  
 20 25 30  
 Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn  
 35 40 45  
 Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr  
 50 55 60  
 Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg  
 65 70 75 80  
 Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile  
 85 90 95  
 Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His  
 100 105 110  
 Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys  
 115 120 125  
 Asn Gly Gly Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn  
 130 135 140  
 Asp Ile Glu Glu Asn Glu Asp Ala Gly Ala Thr Ser Leu Pro Thr Gln  
 145 150 155 160  
 Pro Pro Gln Pro Ser Ser Ser Thr Tyr Asp Pro Gly Asn Met Pro Ser  
 165 170 175  
 Ser Ser Tyr Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala  
 180 185 190  
 Asn Thr Pro  
 195

<210> 28  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 28  
 aaaaggcccc cagggttacg 20  
  
 <210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 29  
 ggagtgggca gcaggtgagc 20  
  
 <210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 30  
 ttaacctgca cagcgacaag t 21  
  
 <210> 31  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 31  
 ttgctgaaga tctcacgctt c 21  
  
 <210> 32  
 <211> 1194  
 <212> DNA  
 <213> Swine  
  
 <220>  
 <221> CDS  
 <222> (1)..(741)  
  
 <400> 32  
 acg gac gag gag ctc cgc agg cgc cag ctg act tgc acc gag gag atg 48  
 Thr Asp Glu Glu Leu Arg Arg Arg Gln Leu Thr Cys Thr Glu Glu Met  
 1 5 10 15  
 gcc cag cga ggg ctg ccg cct gcc ctt gac ccc tgg gag ccg aag gcg 96  
 Ala Gln Arg Gly Leu Pro Pro Ala Leu Asp Pro Trp Glu Pro Lys Ala  
 20 25 30

|                   |                   |                   |                   |                   |                   |                   |                                 |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| gac<br>Asp        | tgg<br>Trp        | gcg<br>Ala<br>35  | ccc<br>Pro        | gca<br>Ala        | ggc<br>Gly        | agc<br>Ser        | ctc<br>Leu<br>40                | agc<br>Ser        | ggt<br>Gly        | gag<br>Glu        | gcc<br>Ala        | ggc<br>Gly<br>45  | cag<br>Gln        | aag<br>Lys        | gat<br>Asp        | 144 |
| gtc<br>Val        | aac<br>Asn<br>50  | ggg<br>Gly        | ccc<br>Pro        | ctg<br>Leu        | agg<br>Arg        | gag<br>Glu<br>55  | ctg<br>Leu                      | cgc<br>Arg        | cca<br>Pro        | agg<br>Arg        | ctc<br>Leu<br>60  | tgc<br>Cys        | cac<br>His        | ctg<br>Leu        | cga<br>Arg        | 192 |
| aaa<br>Lys<br>65  | ggc<br>Gly        | ccc<br>Pro        | cag<br>Gln        | ggt<br>Gly        | tac<br>Tyr<br>70  | ggg<br>Gly        | ttt<br>Phe                      | aac<br>Asn        | ctg<br>Leu        | cac<br>His<br>75  | agc<br>Ser        | gac<br>Asp        | aag<br>Lys        | tcc<br>Ser        | cgg<br>Arg<br>80  | 240 |
| cct<br>Pro        | gga<br>Gly        | cag<br>Gln        | tac<br>Tyr        | atc<br>Ile<br>85  | cgc<br>Arg        | tcc<br>Ser        | gtg<br>Val                      | gac<br>Asp        | cca<br>Pro<br>90  | ggc<br>Gly        | tca<br>Ser        | cct<br>Pro        | gct<br>Ala        | gcc<br>Ala<br>95  | cac<br>His        | 288 |
| tcc<br>Ser        | ggc<br>Gly        | ctc<br>Leu        | cga<br>Arg<br>100 | gcc<br>Ala        | cag<br>Gln        | gac<br>Asp        | cga<br>Arg                      | ctc<br>Leu<br>105 | ata<br>Ile        | gag<br>Glu        | gtg<br>Val        | aac<br>Asn        | ggg<br>Gly<br>110 | cag<br>Gln        | aat<br>Asn        | 336 |
| gtg<br>Val        | gag<br>Glu        | ggg<br>Gly<br>115 | ctg<br>Leu        | cgg<br>Arg        | cac<br>His        | gcg<br>Ala        | gag<br>Glu<br>120               | gtg<br>Val        | gtt<br>Val        | gcc<br>Ala        | tgc<br>Cys        | atc<br>Ile<br>125 | aag<br>Lys        | gcg<br>Ala        | cgg<br>Arg        | 384 |
| gag<br>Glu        | gac<br>Asp<br>130 | gag<br>Glu        | gcc<br>Ala        | cgg<br>Arg        | ctg<br>Leu        | ctg<br>Leu<br>135 | gtg<br>Val                      | gtg<br>Val        | gac<br>Asp        | ccc<br>Pro        | gag<br>Glu<br>140 | acg<br>Thr        | gat<br>Asp        | gtg<br>Val        | tac<br>Tyr        | 432 |
| ttc<br>Phe<br>145 | aag<br>Lys        | cgg<br>Arg        | ctg<br>Leu        | cgg<br>Arg        | gtc<br>Val<br>150 | aca<br>Thr        | ccc<br>Pro                      | acc<br>Thr        | cag<br>Gln        | gag<br>Glu<br>155 | cac<br>His        | atg<br>Met        | gaa<br>Glu        | ggt<br>Gly        | cca<br>Pro<br>160 | 480 |
| ctg<br>Leu        | tca<br>Ser        | tca<br>Ser        | cct<br>Pro        | gtc<br>Val<br>165 | acc<br>Thr        | aat<br>Asn        | ggg<br>Gly                      | acc<br>Thr        | agc<br>Ser<br>170 | tca<br>Ser        | gcc<br>Ala        | cag<br>Gln        | ctc<br>Leu        | aat<br>Asn<br>175 | ggt<br>Gly        | 528 |
| ggc<br>Gly        | tcc<br>Ser        | gtg<br>Val        | tgc<br>Cys<br>180 | tcg<br>Ser        | tcc<br>Ser        | cga<br>Arg        | agt<br>Ser                      | gac<br>Asp<br>185 | ctg<br>Leu        | ccc<br>Pro        | ggc<br>Gly        | tta<br>Leu        | gac<br>Asp<br>190 | aag<br>Lys        | gac<br>Asp        | 576 |
| act<br>Thr        | gag<br>Glu        | gac<br>Asp<br>195 | agc<br>Ser        | agc<br>Ser        | acc<br>Thr        | tgg<br>Trp        | aag<br>Lys<br>200               | cgt<br>Arg        | gac<br>Asp        | cct<br>Pro        | ttc<br>Phe        | cag<br>Gln<br>205 | gag<br>Glu        | agt<br>Ser        | ggc<br>Gly        | 624 |
| ctc<br>Leu        | cac<br>His<br>210 | ctg<br>Leu        | agc<br>Ser        | ccc<br>Pro        | acg<br>Thr        | gcg<br>Ala<br>215 | gct<br>Ala                      | ggg<br>Gly        | gcc<br>Ala        | aag<br>Lys        | gag<br>Glu<br>220 | aag<br>Lys        | gcg<br>Ala        | agg<br>Arg        | gcc<br>Ala        | 672 |
| acc<br>Thr<br>225 | agg<br>Arg        | gtc<br>Val        | aac<br>Asn        | aag<br>Lys        | cgg<br>Arg<br>230 | gcg<br>Ala        | cca<br>Pro                      | cag<br>Gln        | atg<br>Met        | gac<br>Asp<br>235 | tgg<br>Trp        | aac<br>Asn        | cgg<br>Arg        | aag<br>Lys        | cgt<br>Arg<br>240 | 720 |
| gag<br>Glu        | atc<br>Ile        | ttc<br>Phe        | agc<br>Ser        | aac<br>Asn<br>245 | ttc<br>Phe        | tga               | gacccccac cctccgccgc agccgccgcc |                   |                   |                   |                   |                   |                   |                   |                   | 771 |

tgggtccccag ccgggcctcc tctgggcatg gaccttgggc cttgccagaga gcgccccgag 831  
 cctcagtggg ctgcagcggg ggcaccttcg ctcgctaagc cgtgggtggc ccaccacccc 891  
 ccatgaacca gcccgtgccc cagttagccc ccgtcctgcc cccttccac ggggtgctgg 951  
 ggagcgggca gaggaagccc ctgagacggg agggacagag acaccagag aggtgggctg 1011  
 gggagggggag gttgggggtga cccgccaggc cgggcccttg ctgctctgcc tgggcctgct 1071  
 gacttaaagg aatttgtgtt ttggcttttt ttccaacacg agctctggct ccacacatgt 1131

ttccacttaa taccagagcc cccacccccca tccccctcagg acgtgctctc taaataattg 1191  
 caa 1194

<210> 33  
 <211> 246  
 <212> PRT  
 <213> Swine

<400> 33  
 Thr Asp Glu Glu Leu Arg Arg Arg Gln Leu Thr Cys Thr Glu Glu Met  
 1 5 10 15  
 Ala Gln Arg Gly Leu Pro Pro Ala Leu Asp Pro Trp Glu Pro Lys Ala  
 20 25 30  
 Asp Trp Ala Pro Ala Gly Ser Leu Ser Gly Glu Ala Gly Gln Lys Asp  
 35 40 45  
 Val Asn Gly Pro Leu Arg Glu Leu Arg Pro Arg Leu Cys His Leu Arg  
 50 55 60  
 Lys Gly Pro Gln Gly Tyr Gly Phe Asn Leu His Ser Asp Lys Ser Arg  
 65 70 75 80  
 Pro Gly Gln Tyr Ile Arg Ser Val Asp Pro Gly Ser Pro Ala Ala His  
 85 90 95  
 Ser Gly Leu Arg Ala Gln Asp Arg Leu Ile Glu Val Asn Gly Gln Asn  
 100 105 110  
 Val Glu Gly Leu Arg His Ala Glu Val Val Ala Cys Ile Lys Ala Arg  
 115 120 125  
 Glu Asp Glu Ala Arg Leu Leu Val Val Asp Pro Glu Thr Asp Val Tyr  
 130 135 140  
 Phe Lys Arg Leu Arg Val Thr Pro Thr Gln Glu His Met Glu Gly Pro  
 145 150 155 160  
 Leu Ser Ser Pro Val Thr Asn Gly Thr Ser Ser Ala Gln Leu Asn Gly  
 165 170 175  
 Gly Ser Val Cys Ser Ser Arg Ser Asp Leu Pro Gly Leu Asp Lys Asp  
 180 185 190  
 Thr Glu Asp Ser Ser Thr Trp Lys Arg Asp Pro Phe Gln Glu Ser Gly  
 195 200 205  
 Leu His Leu Ser Pro Thr Ala Ala Gly Ala Lys Glu Lys Ala Arg Ala  
 210 215 220  
 Thr Arg Val Asn Lys Arg Ala Pro Gln Met Asp Trp Asn Arg Lys Arg  
 225 230 235 240  
 Glu Ile Phe Ser Asn Phe  
 245

<210> 34  
 <211> 63  
 <212> PRT  
 <213> Swine

<400> 34  
 Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala  
 1 5 10 15  
 Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp  
 20 25 30  
 Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser  
 35 40 45  
 Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His  
 50 55 60

<210> 35  
 <211> 367  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Clone S064  
from BMEC from swine brain

<400> 35

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaataccag | gggtcccca  | gagagatcct | gttcataatt | ttgtcctttt | taacaccatt | 60  |
| tcatttgatc | aagctgatta | gctaagatct | tgttacagca | tttgcagaaa | gcctgaagct | 120 |
| tgatggataa | caacagtttt | aaaccttaag | aaatgacaag | tataaataca | gacacttcaa | 180 |
| tgtagtttta | cattctgagg | caagaaatat | attatacagg | gcctgctgtt | tcctctttaa | 240 |
| tgctctaaaa | gcaccaattt | atgttaaaga | tggcaatgtg | taattataat | cattataatc | 300 |
| tgattagacc | aaacacagga | gcaaagctgt | aattgctttt | agtttttgtt | tttttaacat | 360 |
| gctctgt    |            |            |            |            |            | 367 |

<210> 36

<211> 3071

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Clone S064.3  
from BMEC from swine brain

<400> 36

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| sctwtggcgg  | ggwatctcwa | ggacaaatww  | waatggaatw  | atctctggct  | ggcactcatt  | 60   |
| taattcttaa  | ctatgtaaaa | caacatgagt  | agaaaaaaat  | ttagtgggtat | tatgcctaga  | 120  |
| atagataggt  | gaattccatt | gatgtttatc  | tttgaagacc  | agcttttatgc | gtgaactttt  | 180  |
| catctgwggc  | tttggatcca | aaacatttca  | tgctccagttc | agttctaaag  | gttcttttat  | 240  |
| attttgtcag  | ggtagtctct | ttgagataca  | gcatgatgac  | ttgaatctag  | cagaatattg  | 300  |
| tgctggctac  | ctaaagaagt | gggttcaaat  | cttaatttgg  | ccattacctt  | ttgaccttag  | 360  |
| acagttacta  | ctgtttatgg | tcttcctttc  | gtttttccca  | tgcagaggaa  | cttaaacaaa  | 420  |
| ttatagagtg  | ccaacatgtc | tcttggtttt  | aaaatcgtga  | atctattaaa  | atcccgaatc  | 480  |
| tactaaaaca  | ctattaaaaa | ctggaaaaaa  | aattcaacta  | gggaaagaca  | tgtaatatga  | 540  |
| aatttatttt  | tacctatcat | ttgattccca  | ctttattatc  | ytttcattta  | gtatatgaat  | 600  |
| acaatccaat  | aagaaaatga | aggtcaacta  | ctgccactcc  | acttaaatgt  | aactaatagt  | 660  |
| taatgaagtg  | caaaagagaa | aataagccat  | attgctaaga  | agatgatata  | ttaagctgct  | 720  |
| gataaaatag  | cagtgtgtgt | tgaaaatact  | cttttagaag  | ataccttgct  | tattttcctg  | 780  |
| gcttttatta  | attggatgga | aatgggttagt | ttgatcagag  | tttattggct  | ctagaggctg  | 840  |
| ccccaaattg  | tagctctgtt | tgactttcca  | gtattgaaag  | aatactggaa  | atgtcaatat  | 900  |
| tttacaatag  | tctgtacaaa | tctgaaagta  | gtttatatcc  | atgggttagtt | ttttcagtaa  | 960  |
| cgttccatcc  | ttattcattt | agcattactg  | ttaaagccagg | ttcccaagaa  | gtattttcta  | 1020 |
| agagttccaa  | gtaaccacag | ctacatagag  | aaagccaata  | aaaacaaaac  | tttttagcta  | 1080 |
| cttctctgta  | aatttaaagt | agaaaaaaac  | cagacctaaa  | gtcagctttr  | aatgtatgtg  | 1140 |
| gtctagtga   | atgtttggga | aatgtttatt  | tggagggtta  | gaggcatacc  | gaagcaggag  | 1200 |
| tcaaaacaaa  | gttgggtgga | aagattaaca  | tgaagtaaaa  | aaatcttcag  | tagaaaaatag | 1260 |
| aaagtgttga  | tgaaaacaat | gagttgtccc  | cattcaaggc  | acttaaaatw  | actagaaaaat | 1320 |
| tctgtctttt  | actgtaattg | gatggcctat  | attattttcta | atgtggccaa  | aggactaaag  | 1380 |
| accaatcagg  | tttctagaat | tggggagcgt  | agtcacatag  | aggcatcttt  | tgcatttttt  | 1440 |
| aannnaccag  | taatcttcct | tttcccccta  | gaaakggaga  | aataaaatgt  | tctgtacata  | 1500 |
| tcttttgga   | tagaaagcaa | aattctagaa  | gaatggaagt  | atcctcttac  | accaacttgt  | 1560 |
| agttttaatt  | gaaaaattac | ctcatttttc  | agtcacatag  | gtgctttgct  | cgagtttggt  | 1620 |
| gaatgggtcca | ccatcccat  | aaaaccgcgt  | tcacccaagc  | tgtatttcaa  | atatgcaaaa  | 1680 |
| ttcacagcta  | agggatagca | gtccttgag   | gttttggttt  | ccttcactcg  | cgcttaccac  | 1740 |
| cagcagagct  | aataacgtga | tgtaccaggt  | tgacatactg  | cttcattaaa  | gcacatgggc  | 1800 |
| aaagtgtttag | tcaatattta | attagtttaa  | ttaaaatcaa  | ataagggaaa  | ggaaaaaccc  | 1860 |
| ttagtttga   | ttgagttaca | ttatactgtg  | aatatatttc  | catctgtgtt  | gataagacat  | 1920 |
| caaatgacta  | tcagttgata | ttgattatac  | ataatttatt  | tgcataattct | ggccctattc  | 1980 |
| atgagaggct  | ataatcattt | taatcttaca  | ttttccttca  | ggaaattcag  | ggactctaca  | 2040 |
| gcccctattt  | tgttctcttg | gagtaaawtg  | ttcagtgtag  | tttatgaaaa  | cttttcattt  | 2100 |
| tggtttttaa  | aaaggcttag | ctgctagttc  | attaaaagtg  | tgaaataaaa  | tgatgggtat  | 2160 |
| gatttttcca  | attaatgtta | taaattttas  | cstrtycrtc  | yrwkgtagac  | agcatgttaa  | 2220 |
| aaaaacaaaa  | actaaaagca | attacagctt  | tgctcctgtg  | tttgggtctaa | tcagattata  | 2280 |
| atgattataa  | ttacacattg | ccatcttaac  | ataaattggg  | gcttttagag  | cattaaagag  | 2340 |
| gaaacagcag  | gccctgtata | atatatttct  | tgccctagaa  | tgtaaaacta  | cattgaagtg  | 2400 |
| tctgtattta  | tactgtcat  | ttcttaaggt  | ttaaaactgt  | tggtatccat  | caagcttcag  | 2460 |
| gctttctgca  | aatgctgtaa | caagatctta  | gctaactcagc | ttgrtcacaa  | gaaatgggtg  | 2520 |

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| taaaaaggac | aaaattatga  | acaggatctc | tctgggggac | ccctggtatt | gtacmkrmss | 2580 |
| gggssgaacy | gtctykmag   | ccacaaactg | tgcgtcataa | tcccacccaa | acaactgaca | 2640 |
| tgtgtgtwat | tggttcaata  | cataagcatt | aataaaatta | aaggaacaaa | ttacttaaag | 2700 |
| cagtcacatc | atcacttcct  | caaagtgggt | yaaagcatgt | tcttctaaat | ggaggagttg | 2760 |
| tttaaagaca | tgttttaaat  | tttgatagct | ttactactgt | cataaaatgc | ttctatatgt | 2820 |
| taagtttagg | ttgctgggtac | tcatgatttt | ttacttctgc | aattatgctg | taatgagttg | 2880 |
| cttgcagcc  | tacttaccca  | agtgaagga  | tgctgtttgc | tctggaatgt | tcattcttta | 2940 |
| gacaggtttk | sgctcatttg  | caatcatggg | gcaatacagt | gtaacattca | tttgttttca | 3000 |
| gtcaatagtt | ttatttttgt  | cmcaataaat | aattactttt | ccaaaaaaa  | aaaaaaaaa  | 3060 |
| aaaaaaaaa  | a           |            |            |            |            | 3071 |

<210> 37  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 37  
 taatgcaggg aaaaccacca ttct 24

<210> 38  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 38  
 aaccaagaga catgttggca ct 22

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 39  
 atagcattga cagggaacga ct 22

<210> 40  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial sequence: Primer

<400> 40  
 ctgctagatt caagtcata tgc 23

<210> 41  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 41  
ctcgtgatgg ggctgatctt c

21

<210> 42  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 42  
atctcacacc aatccgggag gt

22

<210> 43  
<211> 540  
<212> DNA  
<213> Swine

<220>  
<221> CDS  
<222> (1)..(537)

|   |     |
|---|-----|
| <400> 43  |     |
| atg ggg ctg atc ttc gct aaa ctg tgg agc ctc ttc tgt aac caa gag | 48  |
| Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu |     |
| 1 5 10 15   |     |
| cac aaa gta att ata gtg gga ctg gat aac gca ggg aag acc act att | 96  |
| His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile |     |
| 20 25 30  |     |
| ctt tat cag ttc tta atg aat gaa gtg gtt cat aca tct cca act ata | 144 |
| Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile |     |
| 35 40 45  |     |
| gga agc aat gtt gaa gaa ata gtt gtg aag aac act cat ttt ctc atg | 192 |
| Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met |     |
| 50 55 60  |     |
| tgg gat att ggt ggt caa gag tca ctg cgg tca tcc tgg aac acg tat | 240 |
| Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr |     |
| 65 70 75 80   |     |
| tat tca aac aca gag ttc atc att ctt gtg gtt gat agc att gac agg | 288 |
| Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg |     |
| 85 90 95  |     |
| gaa cga cta gct att acg aaa gaa gaa tta tac aga atg ttg gct cat | 336 |
| Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His |     |
| 100 105 110   |     |
| gag gat tta cgg aag gct gca gtc ctt atc ttt gcc aat aaa cag gat | 384 |
| Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp |     |
| 115 120 125   |     |
| atg aaa ggg tgc atg aca gca gct gaa atc tcc aaa tac ctc acc ctc | 432 |
| Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu |     |
| 130 135 140   |     |
| agt tca att aag gat cat ccg tgg cat att cag tcc tgc tgt gct tta | 480 |
| Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu |     |
| 145 150 155 160   |     |



<220>

<223> Description of Artificial Sequence: Primer

<400> 46

caattacagc ttgctcctg tg

22

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 47

atagcattga caggaacga ct

22

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 48

gaactgaggg tgaggtattt gg

22

<210> 49

<211> 332

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Clone 5G9 from  
BMEC from swine brain

<400> 49

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tattttgaaa acaattgccc tgggtcasat gttgtccttg ygtatatgtg ggacagccat 120  
caccagccag tatttggcag aaaaatacaa agtgaatacg cccatgcttc agagctttat 180  
caactattgc ttgctgtttc taattttatac aatgatgctg gcatttcagt caggtaataa 240  
taacctttta tgcattctga aaaagaaatg gtggaagtat atcctgctcg gactggcaga 300  
tgtggaagct aattacctga ttgtcagagc gt 332

<210> 50

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 50

tgtatatgtg ggacagccat ca

22

<210> 51

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 51  
gtccgcagcag gatatacttc ca

22

<210> 52  
<211> 2319  
<212> DNA  
<213> Swine

<220>  
<221> CDS  
<222> (480)..(1466)

<400> 52  
agtctctctt cagtccacac aagcctcaga aggggtggcct acggggttga atcgccccctt 60  
caatggcacc tcagagacat ctctgcatcg aaaggcaaac cgaacacgtc cttaaggagg 120  
agacaccaca gaaacatgtt tccaggattc ttttaaggacg ggaaagatag ggaagaaaag 180  
aaacagaact ataggaaata ctttttacga tagtcaagag ggagggagac taggtccaag 240  
gaggggtcag tcggtcctcc ccagttaaca aagggtcattg cttttcaggt ggcataacct 300  
cgattcacct cagggtgctga ttttagataa ggaaccgtaa gaacctgaac cgcctcttgg 360  
gtgtctcctc accccacgca gaagccccac tgccaagacg aagaggaaga gggcatttct 420  
cctccaactc ctgctccgga ggtgccagga atatttttgaa aacaattgcc ctgggtcag 479  
atg ttg tcc ttg tgt ata tgt ggg aca gcc atc acc agc cag tat ttg 527  
Met Leu Ser Leu Cys Ile Cys Gly Thr Ala Ile Thr Ser Gln Tyr Leu  
1 5 10 15  
gca gaa aaa tac aaa gtg aat acg ccc atg ctt cag agc ttt atc aac 575  
Ala Glu Lys Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn  
20 25 30  
tat tgc ttg ctg ttt cta att tat aca atg atg ctg gca ttt cag tca 623  
Tyr Cys Leu Phe Leu Ile Tyr Thr Met Met Leu Ala Phe Gln Ser  
35 40 45  
ggt aat aat aac ctt tta tgc atc ttg aaa aag aaa tgc tgg aag tat 671  
Gly Asn Asn Asn Leu Leu Cys Ile Leu Lys Lys Lys Xaa Trp Lys Tyr  
50 55 60  
atc ctg ctc gga ctg gca gat gtg gaa gct aat tac ctg att gtc aga 719  
Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Leu Ile Val Arg  
65 70 75 80  
gcg tac cag tac aca act cta acc agt gtc cag ctt ttg gat tgc ttt 767  
Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe  
85 90 95  
ggg att cct gtg ttg atg gct ctc tcg tgg ttt att ctt tat gca aga 815  
Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu Tyr Ala Arg  
100 105 110  
tac aga gtg atc cac ttc atc gct gtg gct gtc tgt ctg ttg ggc gta 863  
Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val  
115 120 125  
gga act atg gtt ggt gca gac ata tta gca ggg aga gaa gac aat tca 911  
Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser  
130 135 140

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ggt<br>Gly<br>145 | agt<br>Ser        | gat<br>Asp        | gtg<br>Val        | ctg<br>Leu        | att<br>Ile<br>150 | ggt<br>Gly        | gac<br>Asp        | gtc<br>Val        | ttg<br>Leu        | gtc<br>Val<br>155 | ctt<br>Leu        | ctt<br>Leu        | ggg<br>Gly        | gcc<br>Ala        | tcc<br>Ser<br>160 | 959  |
| ctc<br>Leu        | tat<br>Tyr        | gca<br>Ala        | gtt<br>Val        | tct<br>Ser<br>165 | aat<br>Asn        | gtg<br>Val        | tgt<br>Cys        | gaa<br>Glu        | gaa<br>Glu<br>170 | tac<br>Tyr        | atc<br>Ile        | gtg<br>Val        | aag<br>Lys        | aag<br>Lys<br>175 | ctg<br>Leu        | 1007 |
| agc<br>Ser        | cga<br>Arg        | cag<br>Gln        | gag<br>Glu<br>180 | ttt<br>Phe        | tta<br>Leu        | gga<br>Gly        | atg<br>Met        | gtg<br>Val<br>185 | ggc<br>Gly        | ttg<br>Leu        | ttt<br>Phe        | gga<br>Gly        | aca<br>Thr<br>190 | att<br>Ile        | atc<br>Ile        | 1055 |
| agt<br>Ser        | ggc<br>Gly        | ata<br>Ile<br>195 | cag<br>Gln        | cta<br>Leu        | ttg<br>Leu        | att<br>Ile        | gtg<br>Val<br>200 | gaa<br>Glu        | tat<br>Tyr        | aag<br>Lys        | gat<br>Asp        | att<br>Ile<br>205 | gcc<br>Ala        | agc<br>Ser        | att<br>Ile        | 1103 |
| cac<br>His        | tgg<br>Trp<br>210 | gac<br>Asp        | tgg<br>Trp        | aaa<br>Lys        | att<br>Ile        | gcc<br>Ala<br>215 | cta<br>Leu        | ctg<br>Leu        | ttt<br>Phe        | gta<br>Val        | gca<br>Ala<br>220 | ttt<br>Phe        | gcc<br>Ala        | ctc<br>Leu        | tgt<br>Cys        | 1151 |
| atg<br>Met<br>225 | ttt<br>Phe        | tgc<br>Cys        | ctg<br>Leu        | tac<br>Tyr        | agc<br>Ser<br>230 | ttc<br>Phe        | atg<br>Met        | cca<br>Pro        | ctg<br>Leu        | gtg<br>Val<br>235 | att<br>Ile        | aaa<br>Lys        | gtc<br>Val        | act<br>Thr        | agt<br>Ser<br>240 | 1199 |
| gcc<br>Ala        | act<br>Thr        | tct<br>Ser        | gtc<br>Val        | aac<br>Asn<br>245 | ctg<br>Leu        | ggc<br>Gly        | atc<br>Ile        | ctg<br>Leu        | aca<br>Thr<br>250 | gct<br>Ala        | gac<br>Asp        | ctc<br>Leu        | tat<br>Tyr        | agt<br>Ser<br>255 | ctt<br>Leu        | 1247 |
| ttc<br>Phe        | ttt<br>Phe        | gga<br>Gly        | ctc<br>Leu<br>260 | ttc<br>Phe        | ctg<br>Leu        | ttt<br>Phe        | ggc<br>Gly        | tat<br>Tyr<br>265 | aag<br>Lys        | ttc<br>Phe        | tcg<br>Ser        | gga<br>Gly        | ctc<br>Leu<br>270 | tac<br>Tyr        | atc<br>Ile        | 1295 |
| ctg<br>Leu        | tcc<br>Ser        | ttc<br>Phe<br>275 | gct<br>Ala        | gtc<br>Val        | atc<br>Ile        | atg<br>Met        | gtg<br>Val<br>280 | ggg<br>Gly        | ttc<br>Phe        | att<br>Ile        | ctg<br>Leu        | tac<br>Tyr<br>285 | tgt<br>Cys        | tcc<br>Ser        | acg<br>Thr        | 1343 |
| ccg<br>Pro        | acg<br>Thr<br>290 | cgc<br>Arg        | acg<br>Thr        | gca<br>Ala        | gag<br>Glu        | ccg<br>Pro<br>295 | gct<br>Ala        | gaa<br>Glu        | agc<br>Ser        | agc<br>Ser        | gtg<br>Val<br>300 | cca<br>Pro        | cca<br>Pro        | cca<br>Pro        | gtc<br>Val        | 1391 |
| acc<br>Thr<br>305 | agc<br>Ser        | atc<br>Ile        | ggg<br>Gly        | atc<br>Ile        | gac<br>Asp<br>310 | aac<br>Asn        | ctg<br>Leu        | ggc<br>Gly        | ctg<br>Leu        | aag<br>Lys<br>315 | ctt<br>Leu        | gag<br>Glu        | gag<br>Glu        | aac<br>Asn        | ctc<br>Leu<br>320 | 1439 |
| ccg<br>Pro        | gag<br>Glu        | acc<br>Thr        | cac<br>His        | tcc<br>Ser<br>325 | gtg<br>Val        | gcc<br>Ala        | tta<br>Leu        | tag               | ctggagaaga        | aggcacacac        |                   |                   |                   |                   |                   | 1486 |

atgtactgcg gctttctggg aagccgggag ctatcacctg aataaagcag agcctgttgc 1546  
 ctgctgaggg gacacttgga aaatgatcag atgcagagtg aacactctgg agcactggat 1606  
 tggctctagt ggtagattt tatgaaggaa tacaatcaa tgtatcaaag gtagaagtac 1666  
 caaagtagag cagaagctaa ggcaaggatt gtgtttttgt gtgttttaggg accaatgtgt 1726  
 attaacgtca gggagacaag gtgtgaggcc cacactgggg tctcagaggc acaagatggg 1786  
 aaagcaggat ggggtggata ctcaggtgtg aggcagcctc aggacagggc ctgaaagcag 1846  
 gctgtccagg taggctgggtt ggtcggggag ggggaagagca tcccaggatg gtttgggatt 1906  
 aggtttgctc agttggaggc atctgagttc tgtcctgctg aggcagtgat tgtctcatgg 1966  
 gctagacgag gtctgggtgac tgattgcgta catcaggaag atggagggtg cagcactgga 2026  
 gaaatcctga gatacaagtg tagaaccata gaagcagcac agcggatcct tctcccaatt 2086

gttactacac taatcttagc aaataatgtg ccatgagatt tttatgagac ttcttcaaaa 2146  
 caaagttaac aggaagcatc attatgatat caactaccaa gcagtatgcc mctttacaca 2206  
 gatgctctat gtaaattttg ggggggtaaa aatataataa aggaatcgag ggtaaattgtt 2266  
 catattatta aaaatttttg atttcataga aaaaaaaaaa aaaaaaaaaa aaa 2319

<210> 53  
 <211> 328  
 <212> PRT  
 <213> Swine

<400> 53  
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 1 5 10 15  
 Ala Glu Lys Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn  
 20 25 30  
 Tyr Cys Leu Leu Phe Leu Ile Tyr Thr Met Met Leu Ala Phe Gln Ser  
 35 40 45  
 Gly Asn Asn Asn Leu Leu Cys Ile Leu Lys Lys Lys Xaa Trp Lys Tyr  
 50 55 60  
 Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Leu Ile Val Arg  
 65 70 75 80  
 Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe  
 85 90 95  
 Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu Tyr Ala Arg  
 100 105 110  
 Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val  
 115 120 125  
 Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser  
 130 135 140  
 Gly Ser Asp Val Leu Ile Gly Asp Val Leu Val Leu Leu Gly Ala Ser  
 145 150 155 160  
 Leu Tyr Ala Val Ser Asn Val Cys Glu Tyr Tyr Ile Val Lys Lys Leu  
 165 170 175  
 Ser Arg Gln Glu Phe Leu Gly Met Val Gly Leu Phe Gly Thr Ile Ile  
 180 185 190  
 Ser Gly Ile Gln Leu Leu Ile Val Glu Tyr Lys Asp Ile Ala Ser Ile  
 195 200 205  
 His Trp Asp Trp Lys Ile Ala Leu Leu Phe Val Ala Phe Ala Leu Cys  
 210 215 220  
 Met Phe Cys Leu Tyr Ser Phe Met Pro Leu Val Ile Lys Val Thr Ser  
 225 230 235 240  
 Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu  
 245 250 255  
 Phe Phe Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile  
 260 265 270  
 Leu Ser Phe Ala Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr  
 275 280 285  
 Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Pro Val  
 290 295 300  
 Thr Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu  
 305 310 315 320  
 Pro Glu Thr His Ser Val Ala Leu  
 325

<210> 54  
 <211> 407  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Clone 5E7 from  
 BMEC from swine brain



<400> 54

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agagatctac attataaaat actccgtgaa gaaaaacaca ccaaacgaaa gagattttta 120
gaatttgga cagtttagtcc ctttgtgtaa tctgaactct tctagctgct gaatatcttg 180
aagtcattcc tgttcactga agtctttctg attgagctgg ttgaatactt tgaaaaatga 240
tgcgttctag ctgttgaaat ggatttccca atagggggtc ctgcatatta cctgtatagt 300
agctctatgc atatgtttct gtgcatgctc tctaccagtg tgtaagggtg cactgtattt 360
taactgttgc acttgtcaac ttccaataaa gcatataaaa tgttggt 407
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<210> 55

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: cDNA of  
TSC-22 from BMEC from swine brain

<220>

<221> CDS

<222> (243)..(677)

<400> 55

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agtctagagc ctagtggagc ccggctgccg acctgggagc cttctccgca cagcagttgg 60
atctgcatct tcccgaatc gccaaagcccc agaagccggg tttctttcaa ttaggggtgc 120
tgttttctgt tcctccctga gccgcataaa gctagaagat ttttatctag ctcaaacaag 180
gcctctagaa ttccctcttt tttaattttt ttcctgagag ggtgtttttt ggctgcaatt 240
gc atg aaa tcc caa tgg tgt aga cca gtg gcg atg gat cta gga gtt 287
Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val
1 5 10 15
tac caa ctg aga cat ttt tca att tct ttc ttg tca tcc ttg ctc ggg 335
Tyr Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly
20 25 30
act gaa aac gcc tct gtg aga ctt gac aat agc tct tct ggt gca agt 383
Thr Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser
35 40 45
gtg gta gct att gac aac aaa atc gag caa gct atg gat ctg gtg aaa 431
Val Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys
50 55 60
agc cat ttg atg tat gca gtt aga gag gaa gtg gag gtc ctc aaa gag 479
Ser His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu
65 70 75
caa atc aaa gaa cta ata gag aaa aat tcc cag ctg gag cag gaa aac 527
Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn
80 85 90 95
aat ctg ctg aag aca ctg gcc agt ccg gag cag ctt gcc cag ttc cag 575
Asn Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln
100 105 110
gcc cag ctg cag act ggc tcc ccg ccg gcc acc aca cag ccc cag ggg 623
Ala Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly
115 120 125
acc aca cag ccc ccg gcc cag cca gcg tcc cag ggc tca gga ccg acc 671
Thr Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr
130 135 140
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gcg tag cctcctaggc cccccgcag aactggctgc tgctgtctga accgactgac 727  
Ala 145

cgaccgaccg accggagagg atgtgctggg ggaggggggg gtccgcctcc accacggtca 787  
cccatttcaa tgctcagctg cgaaagagac gtgagactga catatgccat tatctctttt 847  
ttccagtatt aaacctcat gtgcttttgg cttgaagaag tttcttagtt gggcgactta 907  
aagggttaacc agagaattag catggatgta ctgggacctc atgcagcggg gcagatccgt 967  
gagaaatggg ttcatlcatg ctgaggagct gtgtgccttt ccgcccctcc cctgctccgc 1027  
acccccacct ccacccccac ccctaccctt accccccacct ccgagagggtc gtcgtgcttg 1087  
ctcctggcgt gctgcgcgca gtccccaagc cgtggagcgc cactggactc tcctctcgtc 1147  
cctccccac gaggaaccgg aaaggggggt gaaagtcaag accgaagctt catctcacct 1207  
cggaggaggg gaaacgtagg tcattgtaca cgttgacgac tgtcaccaaa atccataaaa 1267  
aaacgaaaca aaaaccaag agtactgtgc ctcttcccaa agcaagggtat gacgcgggac 1327  
tattccagag tgactgaagg gtgacaggta gctggcacct cggctatcaa cgtgaaggyg 1387  
gttttgctca ttgtatattt gtgtatgtag gtgtaactat tttgtacaat agaggactgt 1447  
aactactatt tagcttgtac agactgagat ttagatgttt cattggccgt ctgaagargt 1507  
gtggcttgct ttttatatag agatctacat tataaaatac tccgtgaaga aaaacacacc 1567  
aaacgaaaga gattttaaga atttggcaca gttagtccct ttgtgtaatc tgaactcttc 1627  
tagctgctga atatcttgaa gtcasttctt gttcactgaa gtctttctga ttgagctggg 1687  
tgaatacttt gaaaaatgat gcgttctagc tgttgaaatg gatttcccaa taggggttcc 1747  
tgcatattac ctgtatagta gctctatgca tatgtttctg tgcatgctct ctaccagtt 1807  
gtaagggtgc actgtatttt aactgttgca cttgtcaact ttcaataaag catataaaat 1867  
gttggtvmaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1905

<210> 56  
<211> 144  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: cDNA of  
TSC-22 from BMEC from swine brain

<400> 56  
Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr  
1 5 10 15  
Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr  
20 25 30  
Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val  
35 40 45  
Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser  
50 55 60  
His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln  
65 70 75 80  
Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn  
85 90 95  
Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala  
100 105 110

Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr  
 115 120 125  
 Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala  
 130 135 140

<210> 57  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 57  
 aagaggtgtg gcttgtcttt ta

22

<210> 58  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 58  
 ttttcaaag tattcaacca gctc

24